

SEQUENCE LISTING

<110> Scott, Fred W.

<120> Recombinant Multivalent Viral Vaccine

<130> 18617.0016

<140> 08/552,369

<141> November 3, 1995

<160> 25

<210> 1

<211> 2254

<212> DNA

<213> feline panieukopenia virus

<220>

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Arg Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly
 20 25 30

ggt ggt ggt tct ggg ggt gtg ggg att tct acg ggt act ttc 135
Gly Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe
 35 40 45

aat aat cag acg gaa ttt aaa ttt ttg gaa aac gga tgg gtg gaa 180
Asn Asn Gln Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu
 50 55 60

atc aca gca aac tca agc aga ctt gta cat tta aat atg cca gaa 225

DRAFT - DRAFT

Ile Thr Ala Asn Ser Ser Arg Leu Val His Leu Asn Met Pro Glu			
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Ser Glu Asn Tyr Lys Arg Val Val Val Asn Asn Met Asp Lys Thr			
80	85	90	
gca gtt aaa gga aac atg gct tta gat gac act cat gta caa att	315		
Ala Val Lys Gly Asn Met Ala Leu Asp Asp Thr His Val Gln Ile			
95	100	105	
gta aca cct tgg tca ttg gat gca aat gct tgg gga gtt tgg	360		
Val Thr Pro Trp Ser Leu Val Asp Ala Asn Ala Trp Gly Val Trp			
110	115	120	
ttt aat cca gga gat tgg caa cta att gtt aat act atg agt gag	405		
Phe Asn Pro Gly Asp Trp Gln Leu Ile Val Asn Thr Met Ser Glu			
125	130	135	
ttg cat tta gtt agt ttt gaa caa gaa att ttt aat gtt gtt tta	450		
Leu His Leu Val Ser Phe Glu Gln Glu Ile Phe Asn Val Val Leu			
140	145	150	
aag act gtt tca gaa tct gct act cag cca cca act aaa gtt tat	495		
Lys Thr Val Ser Glu Ser Ala Thr Gln Pro Pro Thr Lys Val Tyr			
155	160	165	
aat aat gat tta act gca tca ttg atg gtt gca tta gat agt aat	540		
Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala Leu Asp Ser Asn			
170	175	180	
aat act atg cca ttt act cca gca gct atg aga tct gag aca ttg	585		
Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser Glu Thr Leu			
185	190	195	
ggt ttt tat cca tgg aaa cca acc ata cca act cca tgg aga tat	630		
Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp Arg Tyr			
200	205	210	
tat ttt caa tgg gat aga aca tta ata cca tct cat act gga act	675		
Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly Thr			
215	220	225	

DRAFT - 060001

agt ggc aca cca aca aat ata tat cat ggt aca gat cca gat gat		720
Ser Gly Thr Pro Thr Asn Ile Tyr His Gly Thr Asp Pro Asp Asp		
230	235	240
gtt caa ttt tat act att gaa aat tct gtg cca gta cac tta cta		765
Val Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu		
245	250	255
aga aca ggt gat gaa ttt gct aca gga aca ttt ttt ttt gat tgt		810
Arg Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Asp Cys		
260	265	270
aaa cca tgt aga cta aca cat aca tgg caa aca aac aga gca ttg		855
Lys Pro Cys Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu		
275	280	285
ggc tta cca cca ttt cta aat tct ttg cct caa tct gaa gga gct		900
Gly Leu Pro Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala		
290	295	300
act aac ttt ggt gat ata gga gtt caa caa gat aaa aga cgt ggt		945
Thr Asn Phe Gly Asp Ile Gly Val Gln Gln Asp Lys Arg Arg Gly		
305	310	315
gta act caa atg gga aat aca gac tat att act gaa gct act att		990
Val Thr Gln Met Gly Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile		
320	325	330
atg aga cca gct gag ggt tat agt gca cca tat tat tct ttt		1035
Met Arg Pro Ala Glu Val Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe		
335	340	345
gaa gcg tct aca caa ggg cca ttt aaa ata cct att gca gca gga		1080
Glu Ala Ser Thr Gln Gly Pro Phe Lys Ile Pro Ile Ala Ala Gly		
350	355	360
cgg ggg gga gcg caa aca gat gaa aat caa gca gca gat ggt gat		1125
Arg Gly Gly Ala Gln Thr Asp Glu Asn Gln Ala Ala Asp Gly Asp		
365	370	375
cca aga tat gca ttt ggt aga caa cat ggt caa aaa act act aca		1170
Pro Arg Tyr Ala Phe Gly Arg Gln His Gly Gln Lys Thr Thr Thr		
380	385	390
aca gga gaa aca cct gag aga ttt aca tat ata gca cat caa gat		1215

PDB ID: 1Q60

Thr	Gly	Glu	Thr	Pro	Glu	Arg	Phe	Thr	Tyr	Ile	Ala	His	Gln	Asp	
				395						400					405
aca	gga	aga	tat	cca	gca	gga	gat	tgg	att	caa	aat	att	aac	ttt	1260
Thr	Gly	Arg	Tyr	Pro	Ala	Gly	Asp	Trp	Ile	Gln	Asn	Ile	Asn	Phe	
				410					415					420	
aac	ctt	cct	gta	aca	aat	gat	aat	gta	ttg	cta	cca	aca	gat	cca	1305
Asn	Leu	Pro	Val	Thr	Asn	Asp	Asn	Val	Leu	Leu	Pro	Thr	Asp	Pro	
				425					430					435	
att	gga	ggt	aaa	aca	gga	atc	aac	tat	act	aat	ata	ttt	aat	act	1350
Ile	Gly	Gly	Lys	Thr	Gly	Ile	Asn	Tyr	Thr	Asn	Ile	Phe	Asn	Thr	
				440					445					450	
tat	ggt	cct	tta	act	gca	tta	aat	aat	gta	cca	cca	gtt	tat	cca	1395
Tyr	Gly	Pro	Leu	Thr	Ala	Leu	Asn	Asn	Val	Pro	Pro	Val	Tyr	Pro	
				455					460					465	
aat	ggt	caa	att	tgg	gat	aaa	gaa	ttt	gat	act	gac	tta	aaa	cca	1440
Asn	Gly	Gln	Ile	Trp	Asp	Lys	Glu	Phe	Asp	Thr	Asp	Leu	Lys	Pro	
				470					475					480	
aga	ctt	cat	gta	aat	gca	cca	ttt	gtt	tgt	caa	aat	aat	tgt	cct	1485
Arg	Leu	His	Val	Asn	Ala	Pro	Phe	Val	Cys	Gln	Asn	Asn	Cys	Pro	
				485					490					495	
ggt	caa	tta	ttt	gta	aaa	gtt	gcg	cct	aat	tta	aca	aat	gaa	tat	1530
Gly	Gln	Leu	Phe	Val	Lys	Val	Ala	Pro	Asn	Leu	Thr	Asn	Glu	Tyr	
				500					505					510	
gat	cct	gat	gca	tct	gct	aat	atg	tca	aga	att	gta	act	tac	tca	1575
Asp	Pro	Asp	Ala	Ser	Ala	Asn	Met	Ser	Arg	Ile	Val	Thr	Tyr	Ser	
				515					520					525	
gat	ttt	tgg	tgg	aaa	ggt	aaa	tta	gta	ttt	aaa	gct	aaa	cta	aga	1620
Asp	Phe	Trp	Trp	Lys	Gly	Lys	Leu	Val	Phe	Lys	Ala	Lys	Leu	Arg	
				530					535					540	
gca	tct	cat	act	tgg	aat	cca	att	caa	caa	atg	agt	att	aat	gta	1665
Ala	Ser	His	Thr	Trp	Asn	Pro	Ile	Gln	Gln	Met	Ser	Ile	Asn	Val	
				545					550					555	
gat	aac	caa	ttt	aac	tat	cta	cca	aat	aat	att	gga	gct	atg	aaa	1710

2000-2001-2002-2003-2004-2005

Asp Asn Gln Phe Asn Tyr Leu Pro Asn Asn Ile Gly Ala Met Lys		
560	565	570
att gta tat gaa aaa tct caa cta gca cct aga aaa tta tat		1752
Ile Val Tyr Glu Lys Ser Gln Leu Ala Pro Arg Lys Leu Tyr		
575	580	
taatatactt actatgttt tatggttatt acatatcaac tagcacctag		1802
aaaattatat taatatactt actatgttt tatgtttatt acatattatt		1852
ttaagattaa ttaaattaca acatagaaat attgtacttg tatttgatat		1902
aggatttaga aggtttgtta tatggtatac aataactgta agaaatagaa		1952
gaacatttag atcatggta gtatggata caataactgt aagaaataga		2002
agaacattta gatcatggtt agtagttgtt ttataaaat gtaattgtaa		2052
actattaatg tatgttgtta tgggtgtgggt gggtgggtgg tttgccctta		2102
gaatatgtta aggacaaaaaa aaatcaataa aagacattta aaacttaatg		2152
gtctcgata ctgtctataa ggtgaactaa ccttaccata agtatcaact		2202
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tg	2254	

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<211> 1575

<212> DNA

<213> rabies virus

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<223>

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DRAFT - 06/04/02

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1	5	10	
cca ttg tgt ttt ggg aaa ttc cct att tac acg ata cta gac Pro Leu Cys Phe Gly Lys Phe Pro Ile Tyr Thr Ile Leu Asp			84
15	20	25	
aag ctt ggt ccc tgg agc ccg att gac ata cat cac ctc agc Lys Leu Gly Pro Trp Ser Pro Ile Asp Ile His His Leu Ser			126
30	35	40	
tgc cca aac aat ttg gta gtg gag gac gaa gga tgc acc aac Cys Pro Asn Asn Leu Val Val Glu Asp Glu Gly Cys Thr Asn			168
45	50	55	
ctg tca ggg ttc tcc tac atg gaa ctt aaa gtt gga tac atc Leu Ser Gly Phe Ser Tyr Met Glu Leu Lys Val Gly Tyr Ile			210
60	65	70	
tta gcc ata aaa atg aac ggg ttc act tgc aca ggc gtt gtg Leu Ala Ile Lys Met Asn Gly Phe Thr Cys Thr Gly Val Val			252
75	80		
acg gag gct gaa acc tac act aac ttc gtt ggt tat gtc aca Thr Glu Ala Glu Thr Tyr Thr Asn Phe Val Gly Tyr Val Thr			294
85	90	95	
acc acg ttc aaa aga aag cat ttc cgc cca aca cca gat gca Thr Thr Phe Lys Arg Lys His Phe Arg Pro Thr Pro Asp Ala			336
100	105	110	
tgt aga gcc gcg tac aac tgg aag atg gcc ggt gac ccc aga Cys Arg Ala Ala Tyr Asn Trp Lys Met Ala Gly Asp Pro Arg			378
115	120	125	
tat gaa gag tct cta cac aat ccg tac cct gac tac cgc tgg Tyr Glu Glu Ser Leu His Asn Pro Tyr Pro Asp Tyr Arg Trp			420
130	135	140	
ctt cga act gta aaa acc acc aag gag tct ctc gtt atc ata Leu Arg Thr Val Lys Thr Lys Glu Ser Leu Val Ile Ile			462
145	150		
tct cca agt gta gca gat ttg gac cca tat gac aga tcc ctt Ser Pro Ser Val Ala Asp Leu Asp Pro Tyr Asp Arg Ser Leu			504

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155	160	165	
cac tcg agg gtc ttc cct agc ggg aag tgc tca gga gta gcg			546
His Ser Arg Val Phe Pro Ser Gly Lys Cys Ser Gly Val Ala			
170	175	180	
gtg tct tct acc tac tgc tcc act aac cac gat tac acc att			588
Val Ser Ser Thr Tyr Cys Ser Thr Asn His Asp Tyr Thr Ile			
185	190	195	
tgg atg ccc gag aat ccg aga cta ggg atg tct tgt gac att			630
Trp Met Pro Glu Asn Pro Arg Leu Gly Met Ser Cys Asp Ile			
200	205	210	
ttt acc aat agt aga ggg aag aga gca tcc aaa ggg agt gag			672
Phe Thr Asn Ser Arg Gly Lys Arg Ala Ser Lys Gly Ser Glu			
215	220		
act tgc ggc ttt gta gat gaa aga ggc cta tat aag tct tta			714
Thr Cys Gly Phe Val Asp Glu Arg Gly Leu Tyr Lys Ser Leu			
225	230	235	
aaa gga gca tgc aaa ctc aag tta tgt gga gtt cta gga ctt			756
Lys Gly Ala Cys Lys Leu Lys Leu Cys Gly Val Leu Gly Leu			
240	245	250	
aga ctt atg gat gga aca tgg gtc gcg atg caa aca tca aat			798
Arg Leu Met Asp Gly Thr Trp Val Ala Met Gln Thr Ser Asn			
255	260	265	
gaa acc aaa tgg tgc gct ccc gat cag ttg gtg aac ctg cac			840
Glu Thr Lys Trp Cys Pro Pro Asp Gln Leu Val Asn Leu His			
270	275	280	
gac ttt cgc tca gac gaa att gag cac ctt gtt gta gag gag			882
Asp Phe Arg Ser Asp Glu Ile Glu His Leu Val Val Glu Glu			
285	290		
ttg gtc agg aag aga gag gag tgt ctg gat gca cta gag tcc			924
Leu Val Arg Lsy Arg Glu Glu Cys Leu Asp Ala Leu Glu Ser			
295	300	305	
atc atg aca aac aag tca gtg agt ttc aga cgt ctc agt cat			966
Ile Met Thr Thr Lys Ser Val Ser Phe Arg Arg Leu Ser His			
310	315	320	

DNA sequence

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Leu Arg Lys Leu Val Pro Gly Phe Gly Lys Ala Tyr Thr Ile		
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Phe Asn Lys Thr Leu Met Glu Ala Asp Ala His Tyr Lys Ser		
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Val Arg Thr Trp Asn Glu Ile Leu Pro Ser Lys Gly Cys Leu		
355	360	
aga gtt ggg ggg agg tgt cat cct cat gtg aac ggg gtg ttt		1134
Arg Val Gly Gly Arg Cys His Pro His Val Asn Gly Val Phe		
365	370	375
ttc aat ggt ata ata tta gga cct gac ggc aat gtc tta atc		1176
Phe Asn Gly Ile Ile Leu Gly Pro Asp Gly Asn Val Leu Ile		
380	385	390
cca gag atg caa tca tcc ctc ctc cag caa cat atg gag ttg		1218
Pro Glu Met Gln Ser Ser Leu Leu Gln Gln His Met Glu Leu		
395	400	405
ttg gaa tcc tcg gtt atc ccc ctt gtg cac ccc ctg gca gac		1260
Leu Glu Ser Ser Val Ile Pro Leu Val His Pro Leu Ala Asp		
410	415	420
ccg tct acc gtt ttc aag gac ggt gac gag gct gag gat ttt		1302
Pro Ser Thr Val Phe Lys Asp Gly Asp Glu Ala Glu Asp Phe		
425	430	
gtt gaa gtt cac ctt ccc gat gtg cac aat cag gtc tca gga		1344
Val Glu Val His Leu Pro Asp Val His Asn Gln Val Ser Gly		
435	440	445
gtt gac ttg ggt ctc ccg aac tgg ggg aag tat gta tta ctg		1386
Val Asp Leu Gly Leu Pro Asn Trp Gly Lys Tyr Val Leu Leu		
450	455	460
agt gca ggg gcc ctg act gcc ttg atg ttg ata att ttc ctg		1428
Ser Ala Gly Ala Leu Thr Ala Leu Met Leu Ile Ile Phe Leu		
465	470	475

atg aca tgt tgt aga aga gtc aat cga tca gaa cct acg caa	1470
Met Thr Cys Cys Arg Arg Val Asn Arg Ser Glu Pro Thr Gln	
480	485
485	490
cac aat ctc aga ggg aca ggg agg gag gtg tca gtc act ccc	1512
His Asn Leu Arg Gly Thr Gly Arg Glu Val Ser Val Thr Pro	
495	500
caa agc ggg aag atc ata tct tca tgg gaa tca cac aag agt	1554
Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Ser His Lys Ser	
505	510
510	515
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ESTIMATE-DNA

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<212> DNA
<213> P11 late promoter and leader sequence
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<213> artificial sequence
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POSSIBLE SEQUENCES

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<212> DNA

<213> artificial sequence

<220> reverse primer

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<212> DNA

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cct cac atc aaa ttg gta atc aac ccc aac aaa ttt cta cat gtt			90
Pro His Ile Lys Leu Val Ile Asn Pro Asn Lys Phe Leu His Val			
20 25	30		
ggc ttc tgc gat aac cct tta atg tgt tat cct gaa tta cta			135
Gly Phe Cys Asp Asn Pro Leu Met Cys Cys Tyr Pro Glu Leu Leu			
35 40	45		
cct gaa ttt ggc acc atg tgg gat tgt gat caa tcg cca ctc caa			180
Pro Glu Phe Gly Thr Met Trp Asp Cys Asp Gln Ser Pro Leu Gln			
50 55	60		
gtc tac ctt gag tca atc ctg ggt gat gat gaa tgg tcc tcc act			225
Val Tyr Leu Glu Ser Ile Leu Gly Asp Asp Glu Trp Ser Ser Thr			
65 70	75		
cat gaa gca att gac cca gtt gtg cca cca atg cat tgg gat gaa			270
His Glu Ala Ile Asp Pro Val Val Pro Pro Met His Trp Asp Glu			
80 85	90		
gcc gga aaa atc ttc caa cca cac cct ggc gtc ctt atg cat cac			315
Ala Gly Lys Ile Phe Gln Pro His Pro Gly Val Leu Met His His			
95 100	105		
ctc atc tgt aag gtt gca gaa gga tgg gac cca aac ctg cca ctt			360
Leu Ile Cys Lys Val Ala Glu Gly Trp Asp Pro Asn Leu Pro Leu			
110 115	120		
ttc cgc ttg gaa gcg gac gat ggt tcc atc acg aca cct gaa cag			405
Phe Arg Leu Glu Ala Asp Asp Gly Ser Ile Thr Thr Pro Glu Gln			
125 130	135		
gga aca atg gtt ggt gga gtc att gct gag ccc aac gcc caa atg			450
Gly Thr Met Val Gly Gly Val Ile Ala Glu Pro Asn Ala Gln Met			
140 145	150		
tca acc gca gct gac atg gcc act ggg aaa agt gtg gac tct gag			495
Ser Thr Ala Ala Asp Met Ala Thr Gly Lys Ser Val Asp Ser Glu			

DRAFT GENOME SEQUENCING

	155	160	165	
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Trp Glu Ala Phe Phe Ser Phe His Thr Ser Val Asn Trp Ser Thr				
170	175	180		
tct gaa act cag ggg aag ata ctc ttt aaa caa tcc tta gga cca				585
Ser Glu Thr Gln Gly Lys Ile Leu Phe Lys Gln Ser Leu Gly Pro				
185	190	195		
ttg ctc aac ccc tac ctt acc cat ctt gca aag ctg tat gtt gct				630
Leu Leu Asn Pro Tyr Leu Thr His Leu Ala Lys Leu Tyr Val Ala				
200	205	210		
tgg tct ggt tct gtt gat gtt agg ttt tct att tct gga tct ggt				675
Trp Ser Gly Ser Val Asp Val Arg Phe Ser Ile Ser Gly Ser Gly				
215	220	225		
gtc ttt gga ggg aaa tta gct gct att gtt gtg ccg cca gga att				720
Val Phe Gly Gly Lys Leu Ala Ala Ile Val Val Pro Pro Gly Ile				
230	235	240		
gat cct gtt caa agt act tca atg ctg caa tat cct cat gtc ctc				765
Asp Pro Val Gln Ser Thr Ser Met Leu Gln Tyr Pro His Val Leu				
245	250	255		
ttt gat gct cgt caa gtt gaa cct gtt atc ttt tcc att ccc gat				810
Phe Asp Ala Arg Gln Val Glu Pro Val Ile Phe Ser Ile Pro Asp				
260	265	270		
cta aga agc acc tta tat cac ctt atg tct gac act gat acc aca				855
Leu Arg Ser Thr Leu Tyr His Leu Met Ser Asp Thr Asp Thr Thr				
275	280	285		
tcg ttg gta atc atg gtg tac aat gat ctt att aac ccc tat gct				900
Ser Leu Val Ile Met Val Tyr Asn Asp Leu Ile Asn Pro Tyr Ala				
290	295	300		
aat gac tca aac tct tcg ggc tgc att gtc act gtg gaa act aaa				945
Asn Asp Ser Asn Ser Ser Gly Cys Ile Val Thr Val Glu Thr Lys				
305	310	315		
ccg ggg cca gat ttc aag ttt cac ctc tta aaa cct cct ggg tct				990
Pro Gly Pro Asp Phe Lys Phe His Leu Leu Lys Pro Pro Gly Ser				
320	325	330		

D
D
E
E
E
D
D

atg tta act cac gga tct atc cca tct gat cta atc cca aaa tca Met Leu Thr His Gly Ser Ile Pro Ser Asp Leu Ile Pro Lys Ser 335 340 345	1035
tct tcg ctt tgg att gga aat cgg ttt tgg tct gac ata acc gat Ser Ser Leu Trp Ile Gly Asn Arg Phe Trp Ser Asp Ile Thr Asp 350 355 360	1080
ttt gta att cgg cct ttt gtg ttc cag gca aat cga cac ttt gat Phe Val Ile Arg Pro Phe Val Phe Gln Ala Asn Arg His Phe Asp 365 370 375	1125
ttc aac caa gag aca gca ggt tgg agc acc cca agg ttt cgc cca Phe Asn Gln Glu Thr Ala Gly Trp Ser Thr Pro Arg Phe Arg Pro 380 385 390	1170
att act atc act atc agt gtt aag gag tca gca aag ctt ggt att Ile Thr Ile Thr Ile Ser Val Lys Glu Ser Ala Lys Leu Gly Ile 395 400 405	1215
gga gtg gcc acc gac tac att gtt ccc ggc ata cca gat gga tgg Gly Val Ala Thr Asp Tyr Ile Val Pro Gly Ile Pro Asp Gly Trp 410 415 420	1260
ccc gac aca aca atc cca ggt gag ttg gta cct gtt ggt gac tat Pro Asp Thr Thr Ile Pro Gly Glu Leu Val Pro Val Gly Asp Tyr 425 430 435	1305
gcc atc act aat ggc acc aac aat gat atc acc aca gct gcg cag Ala Ile Thr Asn Gly Thr Asn Asn Asp Ile Thr Thr Ala Ala Gln 440 445 450	1350
tac gat gca gcc act gag att aga aac aac acc aat ttc aga ggc Tyr Asp Ala Ala Thr Glu Ile Arg Asn Asn Thr Asn Phe Arg Gly 455 460 465	1395
atg tac att tgt ggt tct ctt caa aga gct tgg ggg gat aag aag Met Tyr Ile Cys Gly Ser Leu Gln Arg Ala Trp Gly Asp Lys Lys 470 475 480	1440
att tca aat act gct ttt atc aca acc ggc acg gtt gat gga gcc Ile Ser Asn Thr Ala Phe Ile Thr Thr Gly Thr Val Asp Gly Ala 485 490 495	1485

D 0 9 8 7 6 5 4 3 2 1

aaa ttg ata ccc agt aat acc att gac caa aca aaa att gcc gta	500	505	510	1530
Lys Leu Ile Pro Ser Asn Thr Ile Asp Gln Thr Lys Ile Ala Val				
ttc caa gac aca cat gcg aat aag cat gtc cag acc tcg gac gac	515	520	525	1575
Phe Gln Asp Thr His Ala Asn Lys His Val Gln Thr Ser Asp Asp				
aca ttg gcc ctg ctt ggt tat act ggt att ggt gag gaa gca att	530	535	540	1620
Thr Leu Ala Leu Leu Gly Tyr Thr Gly Ile Gly Glu Glu Ala Ile				
ggt gct gac cgc gat aga gtt gtg cga att agc gtc ctc ccg gaa	545	550	555	1665
Gly Ala Asp Arg Asp Arg Val Val Arg Ile Ser Val Leu Pro Glu				
cgt ggc gca cgt ggt ggc aat cac cca atc ttc cac aaa aac tct	560	565	570	1710
Arg Gly Ala Arg Gly Gly Asn His Pro Ile Phe His Lys Asn Ser				
atc aag ctt ggt tat gta att agg tcc att gat gtg ttc aat tct	575	580	585	1755
Ile Lys Leu Gly Tyr Val Ile Arg Ser Ile Asp Val Phe Asn Ser				
caa att ctg cat acc tct agg caa ctt tcc ctc aat cat tac tta	590	595	600	1800
Gln Ile Leu His Thr Ser Arg Gln Leu Ser Leu Asn His Tyr Leu				
ttg tcg cct gac tcc ttt gct gtc tat agg att att gac tct aat	605	610	615	1845
Leu Ser Pro Asp Ser Phe Ala Val Tyr Arg Ile Ile Asp Ser Asn				
gga tcc tgg ttt gac ata ggc att gat aat gat gga ttt tct ttt	620	625	630	1890
Gly Ser Trp Phe Asp Ile Gly Ile Asp Asn Asp Gly Phe Ser Phe				
gtt ggt gta tca agt att ggt aaa tta gag ttt cct tta act gcc	635	640	645	1935
Val Gly Val Ser Ser Ile Gly Lys Leu Glu Phe Pro Leu Thr Ala				
tcc tac atg gga att caa ttg gca aaa att cga ctt gcc tct aac	650	655	660	1980
Ser Tyr Met Gly Ile Gln Leu Ala Lys Ile Arg Leu Ala Ser Asn				
att agg agt gtg atg aca aaa tta tga		2007		

Ile Arg Ser Val Met Thr Lys Leu
665

<210> 8

<211> 582

<212> DNA

<213> artificial sequence

<220> hemagglutinin left arm

<223>

<400> 1

attaaacgca aatatccatg gaaaacgcgc agtatacaga cgattttta	50
cagtatttgg agagtttat aggaagtata tagagtagaa ccagaatttt	100
gtaaaaataa atcacattt tatactaata taaaacaact atcgatagtt	150
atattgctac tatcgatagt atatacaacc aaacctcatc ctacacagat	200
atcaaaaaaa ctaggcgatg atgctactct atcgtgtaat agaaaacaata	250
cacatggata tcttgtcatg agttcttggt ataagaaacc agactccatt	300
attctcttag cagccaaaaa cgatgtcgta tactttgatg attatacagc	350
ggataaaagta tcatacgatt caccgtatga tactctagct acaattatata	400
caattaaatc attgacatct gcagatgcag gtacttatat atgcgcattc	450
tttataacat caacaaatga tacggataaa atagattatg aagaataactt	500
catagatttgc ttgttaatc cagctaattgt atccactatt gacgcgattc	550
tatcaggatc taatttctcc gtgataggta tc	582

<210> 9

<211> 447

<212> DNA

<213> artificial sequence

<220> hemagglutinin right arm

<223>

<400> 1

ctctagcgcc taaccccagg cgaccgacga caacctttat gatacatata	50
atgaaccaat atctgtatca tcctcgatac caacaacggt agaaaagtgtt	100
acaatatcta ctacaaaata tacaactagt gactttatag agatatttgg	150

cattgtttca ctaatttat tattggccgt ggcgatttc tgtattat 200
tatttctgtc gtggacggc tcgtaaacaa gaaacaaata tattatagat 250
ttaactcag ataaatgtct ggaataatta aatctatcg 300
ccatctggtt ccggcaagac agctatacg aggagactct tacaagat 350
tggaaatata ttggatgg tggtatcca taccactaga ttccctcg 400
ctatggaacg agaagggtgc gactaccatt acgttaacag agaggcc 447

<210> 10

<211> 40

<212> DNA

<213> artificial sequence

<220> primer P3

<223>

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gatacctatc acggagaaat tagatcctga tagaatcg 40

<210> 11

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<213> artificial sequence

<220> primer P1

<223>

<400> 1

attaaacgca aatatccatg gg 22

<210> 12

<211> 27

<212> DNA

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T040208-PEP001

EST-2000-0000

<213> artificial sequence
<220> primer F2
<223>
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gcggtaaccct ggggttaggc gatagag 27

<210> 13
<211> 20
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<213> artificial sequence
<220> primer P5
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atttctccgt gataggtatc 20

<210> 14
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<210> 15
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FOLIO NO. 400-1234567890

<212> DNA

<213> artificial sequence

<220> primer P2

<223>

<400> 1

gcgtcgaagt ttgagcatgt gc 22

<210> 16

<211> 40

<212> DNA

<213> artificial sequence

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<223>

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<210> 17

<211> 840

<212> DNA

<213> feline infectious peritonitis virus

<220>

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atg aag tac att ttg cta ata ctc gcg tgc ata att gca tgc gtt 96

Met Lys Tyr Ile Leu Leu Ile Leu Ala Cys Ile Ile Ala Cys Val
 1 5 10 15
 tat ggt gaa cgc tac tgt gcc atg caa gac agt ggc ttg cag tgt 141
 Tyr Gly Glu Arg Tyr Cys Ala Met Gln Asp Ser Gly Leu Gln Cys
 20 25 30
 att aat ggc aca aat tca aga tgt caa acc tgc ttt gaa cgt ggt 186
 Ile Gln Gly Thr Gln Ser Arg Cys Gln Thr Cys Phe Glu Arg Gly
 35 40 45
 gat ctt att tgg cat ctt gct aac tgg aac ttc agc tgg tct gta 231
 Asp Leu Ile Trp His Leu Ala Asn Trp Asn Phe Ser Trp Ser Val
 50 55 60
 ata ttg att gtt ttt ata aca gtg tta caa tat ggc aga cca caa 276
 Ile Leu Ile Val Phe Ile Thr Val Leu Gln Tyr Gly Arg Pro Gln
 65 70 75
 ttt agc tgg ctc gtt tat ggc att aaa atg ctg atc atg tgg cta 321
 Phe Ser Trp Leu Val Tyr Gly Ile Lys Met Leu Ile Met Trp Leu
 80 85 90
 tta tgg cct att gtt cta gcg ctt acg att ttt aat gca tac tct 366
 Leu Trp Pro Ile Val Leu Ala Leu Thr Ile Phe Asn Ala Tyr Ser
 95 100 105
 gag tac caa gtt tcc aga tat gta atg ttc ggc ttt agt gtt gca 411
 Glu Tyr Gln Val Ser Arg Tyr Val Met Phe Gly Phe Ser Val Ala
 110 115 120
 ggt gca gtt gta acg ttt gca ctt tgg atg atg tat ttt gtg aga 456
 Gly Ala Val Val Thr Phe Ala Leu Trp Met Met Tyr Phe Val Arg
 125 130 135
 tct gtt cag cta tat aga aga acc aaa tca tgg tgg tct ttt aat 501
 Ser Val Gln Leu Tyr Arg Axa Thr Lys Ser Trp Trp Ser Phe Asn
 140 145 150
 cct gag act aat gca att ctt tgt gtt aat gca ttg ggt aga agt 546
 Pro Glu Thr Asn Ala Ile Leu Cys Val Asn Ala Leu Gly Arg Ser
 155 160 165
 tat gtg ctt ccc tta gat ggt act cct aca ggt gtt acc ctt act 591
 Tyr Val Leu Pro Leu Asp Gly Thr Pro Thr Gly Val Thr Leu Thr

170	175	180	
ctt ctt tca gga aat cta tat gct gaa ggt ttc aaa atg gct ggt			636
Leu Leu Ser Gly Asn Leu Tyr Ala Glu Gly Phe Lys Met Ala Gly			
185	190	195	
ggt tta acc atc gag cat ttg cct aaa tac gtc atg att gct aca			681
Gly Leu Thr Ile Glu His Leu Pro Lys Tyr Val Met Ile Ala Thr			
200	205	210	
cct agt aga acc atc gtt tat aca tta gtt gga aaa caa tta aaa			726
Pro Ser Arg Thr Ile Val Tyr Thr Ile Val Gly Lys Gln Leu Lys			
215	220	225	
gca act act gcc aca gga tgg gct tac tac gta aaa tct aaa gct			771
Ala Thr Thr Ala Thr Gly Trp Ala Tyr Tyr Val Lys Ser Lys Ala			
230	235	240	
ggt gat tac tca aca gaa gca cgt act gac aat ttg agt gaa cat			816
Gly Asp Tyr Ser Thr Glu Ala Arg Thr Asp Asn Leu Ser Glu His			
245	250	255	
gaa aaa tta tta cat atg gtg taa	840		
Glu Lys Leu Leu His Met Val			
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<210> 18			
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Met Ala Thr Gln Gly Gln Arg Val Asn Trp Gly Asp Glu Pro Ser			
1	5	10	15
aaa aga cgt ggt cgt tct aac tct cgt ggt cgg aag aat aat gat			90
Lys Arg Arg Gly Arg Ser Asn Ser Arg Gly Arg Lys Asn Asn Asp			

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	20	25	30
ata cct ttg tca ttc tac aac ccc att acc ctc gaa caa gga tct			135
Ile Pro Leu Ser Phe Tyr Asn Phe Ile Thr Leu Glu Gln Glu Ser			
	35	40	45
aaa ttt tgg aat tta tgt ccg aga gac ctt gtt ccc aaa gga ata			180
Lys Phe Trp Asn Leu Cys Pro Arg Asp Leu Val Pro Lys Gly Ile			
	50	55	60
ggt aat aag gat caa caa att ggt tat tgg aat aga cag att cgt			225
Gly Asn Lys Asp Gln Gln Ile Gly Tyr Trp Asn Arg Gln Ile Arg			
	65	70	75
tat cgt att gta aaa ggc cag cgt aag gaa ctc gct gag agg tgg			270
Tyr Arg Ile Val Lys Gly Gln Arg Lys Glu Leu Ala Glu Arg Trp			
	80	85	90
ttc ttt tac ttc tta ggt aca gga cct cat gct gat gct aaa ttc			315
Phe Phe Tyr Phe Leu Gly Thr Gly Phe His Ala Asp Ala Lys Phe			
	95	100	105
aaa gac aag att gat gga gtc ttc tgg gtt gca agg gat ggt gcc			360
Lys Asp Lys Ile Asp Gly Val Phe Trp Val Ala Arg Asp Gly Ala			
	110	115	120
atg aac aag ccc aca acg ctt ggc act cgt gga acc aat aac gaa			405
Met Asn Lys Pro Thr Thr Leu Gly Thr Arg Gly Thr Asn Asn Glu			
	125	130	135
tcc aaa cca ctg aga ttt gat ggt aag ata ccg cca cag ttt cag			450
Ser Lys Pro Leu Arg Phe Asp Gly Lys Ile Pro Pro Gln Phe Gln			
	140	145	150
ctt gaa gtg aac cgt tct agg aac aat tca agg tct ggt tct cag			495
Leu Glu Val Asn Arg Ser Arg Asn Asn Ser Arg Ser Gly Ser Gln			
	155	160	165
tct aga tct gtt tca aga aac aga tct caa tct aga gga aga cac			540
Ser Arg Ser Val Ser Arg Asn Arg Ser Gln Ser Arg Gly Arg His			
	170	175	180
cat tcc aat aac cag aat aat gtt gag gat aca att gta gcc			585
His Ser Asn Asn Gln Asn Asn Val Glu Asp Thr Ile Val Ala			
	185	190	195

D 60 2860 2860 2860 2860

gtg ctt gaa aaa tta ggt gtt act gac aaa caa agg tca cgt tct 630
Val Leu Glu Lys Leu Gly Val Thr Asp Lys Gln Arg Ser Arg Ser
200 205 210

aaa cct aga gaa cgt agt gat tcc aaa cct agg gac aca aca cct 675
Lys Pro Arg Glu Arg Ser Asp Ser Lys Pro Arg Asp Thr Thr Pro
215 220 225

aag aat gcc aac aaa cac acc tgg aag aaa act gca ggc aag gga 720
Lys Asn Ala Asn Lys His Thr Trp Lys Lys Thr Ala Gly Lys Gly
230 235 240

gat gtg aca act ttc tat ggt gct aga agt agt tca gct aac ttt 765
Asp Val Thr Thr Phe Tyr Gly Ala Arg Ser Ser Ser Ala Asn Phe
245 250 255

ggt gat agt gat ctc gtt gcc aat ggt aac gct gcc aaa tgc tac 810
Gly Asp Ser Asp Leu Val Ala Asn Gly Asn Ala Ala Lys Cys Tyr
260 265 270

cct cag ata gct gaa tgt gtt cca tca gtg tct agc ata atc ttt 855
Pro Gln Ile Ala Glu Cys Val Pro Ser Val Ser Ser Ile Ile Phe
275 280 285

ggc agt caa tgg tct gct gaa gaa gct ggt gat caa gtg aaa gtc 900
Gly Ser Gln Trp Ser Ala Glu Glu Ala Gly Asp Gln Val Lys Val
290 295 300

acg ctc act cac acc tac tac ctg cca aag gat gat gcc aaa act 945
Thr Leu Thr His Thr Tyr Tyr Leu Pro Lys Asp Asp Ala Lys Thr
305 310 315

agt caa ttc cta gaa cag att gac gct tac aag cga cct tct gaa 990
Ser Gln Phe Leu Glu Gln Ile Asp Ala Tyr Lys Atg Pro Ser Glu
320 325 330

gtg gct aag gat cag agg caa aga aga tcc cgt tct aag tct gct 1035
Val Ala Lys Asp Gln Arg Gln Arg Arg Ser Arg Ser Lys Ser Ala
335 340 345

gat aag aag cct gag gag ttg tct gta act ctt gtg gag gca tac 1080
Asp Lys Lys Pro Glu Glu Lys Ser Val Thr Leu Val Glu Ala Tyr
350 355 360

aca gat gtg ttt gat gac aca cag gtt gag atg att gat gag gtt 1125

Thr Asp Val Phe Asp Asp Thr Gln Val Glu Met Ile Asp Glu Val
365 370 375

acg aac taa acgcatgctc 1144

Thr Asn

377

<210> 19

<211> 1979

<212> DNA

<213> feline leukemia virus

<220>

<223>

<400> 1

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atg gaa agt cca acg cac cca aaa ccc tct aaa gat aag act ctc      95
Met Glu Ser Pro Thr His Pro Lys Pro Ser Lys Asp Lys Thr Leu
   1           5           10          15

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tcg tgg aac tta gcg ttt ctg gtg ggg atc tta ttt aca ata gac 140
Ser Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp
                           20                      25                      30

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ata gga atg gcc aat cct agt cca cac caa ata tat aat gta act 185
Ile Gly Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr
            35           .           40           45

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tgg gta ata acc aat gta caa act aac acc caa gct aac gcc acc 230
Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr
50 55 60

tct atg tta gga acc tta acc gat gcc tac cct acc cta cat gtt 275
Ser Met Leu Gly Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val
65 70 75

gac tta tgt gac cta gtg gga gac acc tgg gaa cct ata gtc cta 320
Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Ile Val Leu

DRAFT - 1999

80	85	90
aac cca acc aat gta aaa cac ggg gca cgt tac tcc tcc tca aaa		365
Asn Pro Thr Asn'Val Lys His Gly Ala Arg Tyr Ser Ser Ser Lys		
95	100	105
tat gga tgt aaa act aca gat aga aaa aaa cag caa cag aca tac	410	
Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln Thr Tyr		
110	115	120
ccc ttt tac gtc tgc ccc gga cat gcc ccc tcg ttg ggg cca aag	455	
Pro Phe Tyr Val Cys Pro Gly His Ala Pro Ser Leu Gly Pro Lys		
125	130	135
gga aca cat tgt gga ggg gca caa gat ggg ttt tgt gcc gca tgg	500	
Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp		
140	145	150
gga tgt gag acc acc gga gaa gct tgg tgg aag ccc acc tcc tca	545	
Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser		
155	160	165
tgg gac tat atc aca gta aaa aga ggg agt agt cag gac aat agc	590	
Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser		
170	175	180
tgt gag gga aaa tgc aac ccc ctg gtt ttg cag ttc acc cag aag	635	
Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys		
185	190	195
gga aga caa gcc tct tgg gac gga cct aag atg tgg gga ttg cga	680	
Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg		
200	205	210
cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc	725	
Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser		
215	220	225
cgg cag gta tca acc att acg ccg cct cag gca atg gga cca aac	770	
Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn		
230	235	240
cta gtc tta cct gat caa aaa ccc cca tcc cga caa tct caa aca	815	
Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr		

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245	250	255
ggg tcc aaa gtg gcg acc cag agg ccc caa acg aat gaa agc gcc 860		
Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala		
260	265	270
cca agg tct gtt gcc ccc acc acc atg ggt ccc aaa cgg att ggg 905		
Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly		
275	280	285
acc gga gat agg tta ata aat tta gta caa ggg aca tac cta gcc 950		
Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala		
290	295	300
tta aat gcc acc gac ccc aac aaa act aaa gac tgt tgg ctc tgc 995		
Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys		
305	310	315
ctg gtt tct cga cca ccc tat tac gaa ggg att gca atc tta ggt 1040		
Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly		
320	325	330
acc tac agc aac caa aca aac ccc cca tcc tgc cta tct act 1085		
Asn Tyr Ser Asn Gln Thr Asn Pro Pro Ser Cys Leu Ser Ile		
335	340	345
ccg caa cac aaa cta act ata tct gaa gta tca ggg caa gga atg 1130		
Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met		
350	355	360
tgc ata ggg act gtt cct aaa acc cac cag gct ttg tgc aat aag 1175		
Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys		
365	370	375
aca caa cag gga cat aca ggg gcg cac tat cta gcc gcc ccc aac 1220		
Thr Gln Gln Gly His Thr Gly Ala His Tyr Leu Ala Ala Pro Asn		
380	385	390
ggc acc tat tgg gcc tgt aac act gga ctc acc cca tgc att tcc 1265		
Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu Thr Pro Cys Ile Ser		
395	400	405

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Met Ala Val Leu Asn Trp Thr Ser Asp Phe Cys Val Leu Ile Glu
410 415 420

tta tgg ccc aga gtg act tac cat caa ccc gaa tat gtg tac aca 1355
Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr Val Tyr Thr
425 430 435

cat ttt gcc aaa gct gtc agg ttc cga aga gaa cca ata tca cta 1400
His Phe Ala Lys Ala Val Arg Phe Arg Axg Glu Pro Ile Ser Leu
440 445 450

acg gtt gcc ctt atg ttg gga gga ctt act gta ggg ggc ata gcc 1445
Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile Ala
455 460 465

gcg ggg gtc gga aca ggg act aaa gcc ctc ctt gaa aca gcc cag 1490
Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln
470 475 480

ttc aga caa cta caa atg gcc atg cac aca gac atc cag gcc cta 1535
Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu
485 490 495

gaa gaa tca att agt gcc tta gaa aag tcc ctg acc tcc ctt tct 1580
Glu Glu Ser Ile Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser
500 505 510

gaa gta gtc tta caa aac aga cgg ggc cta gat att cta ttc tta 1625
Glu Val Val Leu Gln Asn Arg Arg Glu Leu Asp Ile Leu Phe Leu
515 520 525

caa gag gga ggg ctc tgt gcc gca ttg aaa gaa gaa tgt tgc ttc 1670
Gln Glu Gly Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe
530 535 540

tat gcg gat cac acc gga ctc gtc cga gac aat atg gcc aaa tta 1715
Tyr Ala Asp His Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu
545 550 555

aga gaa aga cta aaa cag cgg caa caa ctg ttt gac tcc caa cag 1760
Arg Glu Arg Leu Lys Gln Arg Gln Gln Leu Phe Asp Ser Gln Gln
560 565 570

09873881-0E0401

gga tgg ttt gaa gga tgg ttc aac aag tcc ccc tgg ttt aca acc 1805
Gly Trp Phe Glu Gly Trp Phe Asn Lys Ser Pro Trp Phe Thr Thr
575 580 585

cta att tcc tcc att atg ggc ccc tta cta atc cta ctc cta att 1850
Leu Ile Ser Ser Ile Met Gly Pro Leu Leu Ile Leu Leu Ile
590 595 600

ctc ctc ttc ggc cca tgc atc ctt aac cga tta gta caa ttc gta
1895 Leu Leu Phe Gly Pro Cys Ile Leu Asn Arg Leu Val Gln Phe
Val
605 610 615

aaa gac aga ata tct gtg gta cag gct tta att tta acc caa cag
1940 Lys Asp Axa Ile Ser Val Val Gln Ala Leu Ile Leu Thr Gln
Gln
620 625 630

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635 640

<210> 20

<211> 584

<212> PRT

<213> feline panleukopenia peritonitis virus

<220>

<223>

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20 25 30

Gly Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe
35 40 45

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Asn	Asn	Gln	Thr	Glu	Phe	Lys	Phe	Leu	Glu	Asn	Gly	Trp	Val	Glu
														50
														55
														60
Ile	Thr	Ala	Asn	Ser	Ser	Arg	Leu	Val	His	Leu	Asn	Met	Pro	Glu
														65
														70
														75
Ser	Glu	Asn	Tyr	Lys	Arg	Val	Val	Val	Asn	Asn	Met	Asp	Lys	Thr
														80
														85
														90
Ala	Val	Lys	Gly	Asn	Met	Ala	Leu	Asp	Asp	Thr	His	Val	Gln	Ile
														95
														100
														105
Val	Thr	Pro	Trp	Ser	Leu	Val	Asp	Ala	Asn	Ala	Trp	Gly	Val	Trp
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														115
														120
Phe	Asn	Pro	Gly	Asp	Trp	Gln	Leu	Ile	Val	Asn	Thr	Met	Ser	Glu
														125
														130
														135
Leu	His	Leu	Val	Ser	Phe	Glu	Gln	Glu	Ile	Phe	Asn	Val	Val	Leu
														140
														145
														150
Lys	Thr	Val	Ser	Glu	Ser	Ala	Thr	Gln	Pro	Pro	Thr	Lys	Val	Tyr
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														160
														165
Asn	Asn	Asp	Leu	Thr	Ala	Ser	Leu	Met	Val	Ala	Leu	Asp	Ser	Asn
														170
														175
														180
Asn	Thr	Met	Pro	Phe	Thr	Pro	Ala	Ala	Met	Arg	Ser	Glu	Thr	Leu
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														190
														195
Gly	Phe	Tyr	Pro	Trp	Lys	Pro	Thr	Ile	Pro	Thr	Pro	Trp	Arg	Tyr
														200
														205
														210
Tyr	Phe	Gln	Trp	Asp	Arg	Thr	Leu	Ile	Pro	Ser	His	Thr	Gly	Thr
														215
														220
														225
Ser	Gly	Thr	Pro	Thr	Asn	Ile	Tyr	His	Gly	Thr	Asp	Pro	Asp	Asp
														230
														235
														240
Val	Gln	Phe	Tyr	Thr	Ile	Glu	Asn	Ser	Val	Pro	Val	His	Leu	Leu
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														250
														255
Arg	Thr	Gly	Asp	Glu	Phe	Ala	Thr	Gly	Thr	Phe	Phe	Phe	Asp	Cys
														260
														265
														270

D9923688-000001

Lys	Pro	Cys	Arg	Leu	Thr	His	Thr	Trp	Gln	Thr	Asn	Axg	Ala	Leu
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Gly	Leu	Pro	Pro	Phe	Leu	Asn	Ser	Leu	Pro	Gln	Ser	Glu	Gly	Ala
				290					295					300
Thr	Asn	Phe	Gly	Asp	Ile	Gly	Val	Gln	Gln	Asp	Lys	Arg	Arg	Gly
				305					310					315
Val	Thr	Gln	Met	Gly	Asn	Thr	Asp	Tyr	Ile	Thr	Glu	Ala	Thr	Ile
				320					325					330
Met	Arg	Pro	Ala	Glu	Val	Gly	Tyr	Ser	Ala	Pro	Tyr	Tyr	Ser	Phe
				335					340					345
Glu	Ala	Ser	Thr	Gln	Gly	Pro	Phe	Lys	Ile	Pro	Ile	Ala	Ala	Gly
				350					355					360
Arg	Gly	Gly	Ala	Gln	Thr	Asp	Glu	Asn	Gln	Ala	Ala	Asp	Gly	Asp
				365					370					375
Pro	Arg	Tyr	Ala	Phe	Gly	Arg	Gln	His	Gly	Gln	Lys	Thr	Thr	Thr
				380					385					390
Thr	Gly	Glu	Thr	Pro	Glu	Arg	Phe	Thr	Tyr	Ile	Ala	His	Gln	Asp
				395					400					405
Thr	Gly	Arg	Tyr	Pro	Ala	Gly	Asp	Trp	Ile	Gln	Asn	Ile	Asn	Phe
				410					415					420
Asn	Leu	Pro	Val	Thr	Asn	Asp	Asn	Val	Leu	Leu	Pro	Thr	Asp	Pro
				425					430					435
Ile	Gly	Gly	Lys	Thr	Gly	Ile	Asn	Tyr	Thr	Asn	Ile	Phe	Asn	Thr
				440					445					450
Tyr	Gly	Pro	Leu	Thr	Ala	Leu	Asn	Asn	Val	Pro	Pro	Val	Tyr	Pro
				455					460					465
Asn	Gly	Gln	Ile	Trp	Asp	Lys	Glu	Phe	Asp	Thr	Asp	Leu	Lys	Pro
				470					475					480

DRAFT - DRAFT

Arg Leu His Val Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro
485 490 495

Gly Gln Leu Phe Val Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr
500 505 510

Asp Pro Asp Ala Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser
515 520 525

Asp Phe Trp Trp Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg
530 535 540

Ala Ser His Thr Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val
545 550 555

Asp Asn Gln Phe Asn Tyr Leu Pro Asn Asn Ile Gly Ala Met Lys
560 565 570

Ile Val Tyr Glu Lys Ser Gln Leu Ala Pro Arg Lys Leu Tyr
575 580

<210> 21

<211> 524

<212> PRT

<213> rabies virus

<220>

<223>

<400> 1

Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe
1 5 10

Pro Leu Cys Phe Gly Lys Phe Pro Ile Tyr Thr Ile Leu Asp
15 20 25

Lys Leu Gly Pro Trp Ser Pro Ile Asp Ile His His Leu Ser
30 35 40

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Cys	Pro	Asn	Asn	Leu	Val	Val	Glu	Asp	Glu	Gly	Cys	Thr	Asn
	45						50					55	
Leu	Ser	Gly	Phe	Ser	Tyr	Met	Glu	Leu	Lys	Val	Gly	Tyr	Ile
	60							65					70
Leu	Ala	Ile	Lys	Met	Asn	Gly	Phe	Thr	Cys	Thr	Gly	Val	Val
				75					80				
Thr	Glu	Ala	Glu	Thr	Tyr	Thr	Asn	Phe	Val	Gly	Tyr	Val	Thr
	85				90					95			
Thr	Thr	Phe	Lys	Arg	Lys	His	Phe	Arg	Pro	Thr	Pro	Asp	Ala
	100					105				110			
Cys	Arg	Ala	Ala	Tyr	Asn	Trp	Lys	Met	Ala	Gly	Asp	Pro	Arg
	115						120				125		
Tyr	Glu	Glu	Ser	Leu	His	Asn	Pro	Tyr	Pro	Asp	Tyr	Arg	Trp
		130						135			140		
Leu	Arg	Thr	Val	Lys	Thr	Thr	Lys	Glu	Ser	Leu	Val	Ile	Ile
				145					150				
Ser	Pro	Ser	Val	Ala	Asp	Leu	Asp	Pro	Tyr	Asp	Arg	Ser	Leu
	155				160				165				
His	Ser	Arg	Val	Phe	Pro	Ser	Gly	Lys	Cys	Ser	Gly	Val	Ala
	170					175				180			
Val	Ser	Ser	Thr	Tyr	Cys	Ser	Thr	Asn	His	Asp	Tyr	Thr	Ile
	185						190			195			
Trp	Met	Pro	Glu	Asn	Pro	Arg	Leu	Gly	Met	Ser	Cys	Asp	Ile
		200					205			210			
Phe	Thr	Asn	Ser	Arg	Gly	Lys	Arg	Ala	Ser	Lys	Gly	Ser	Glu
			215					220					
Thr	Cys	Gly	Phe	Val	Asp	Glu	Arg	Gly	Leu	Tyr	Lys	Ser	Leu
	225				230				235				
Lys	Gly	Ala	Cys	Lys	Leu	Lys	Leu	Cys	Gly	Val	Leu	Gly	Leu
		240				245				250			

Arg Leu Met Asp Gly Thr Trp Val Ala Met Gln Thr Ser Asn
255 260 265

Glu Thr Lys Trp Cys Pro Pro Asp Gln Leu Val Asn Leu His
270 275 280

Asp Phe Arg Ser Asp Glu Ile Glu His Leu Val Val Glu Glu
285 290

Leu Val Arg Lsy Arg Glu Glu Cys Leu Asp Ala Leu Glu Ser
295 300 305

Ile Met Thr Thr Lys Ser Val Ser Phe Arg Arg Leu Ser His
310 315 320

Leu Arg Lys Leu Val Pro Gly Phe Gly Lys Ala Tyr Thr Ile
325 330 335

Phe Asn Lys Thr Leu Met Glu Ala Asp Ala His Tyr Lys Ser
340 345 350

Val Arg Thr Trp Asn Glu Ile Leu Pro Ser Lys Gly Cys Leu
355 360

Arg Val Gly Gly Arg Cys His Pro His Val Asn Gly Val Phe
365 370 375

Phe Asn Gly Ile Ile Leu Gly Pro Asp Gly Asn Val Leu Ile
380 385 390

Pro Glu Met Gln Ser Ser Leu Leu Gln Gln His Met Glu Leu
395 400 405

Leu Glu Ser Ser Val Ile Pro Leu Val His Pro Leu Ala Asp
410 415 420

Pro Ser Thr Val Phe Lys Asp Gly Asp Glu Ala Glu Asp Phe
425 430

Val Glu Val His Leu Pro Asp Val His Asn Gln Val Ser Gly
435 440 445

Val Asp Leu Gly Leu Pro Asn Trp Gly Lys Tyr Val Leu Leu
450 455 460

Ser Ala Gly Ala Leu Thr Ala Leu Met Leu Ile Ile Phe Leu
465 470 475

Met Thr Cys Cys Arg Arg Val Asn Arg Ser Glu Pro Thr Gln
480 485 490

His Asn Leu Arg Gly Thr Gly Arg Glu Val Ser Val Thr Pro
495 500

Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Ser His Lys Ser
505 510 515

Gly Gly Glu Thr Arg Leu
520 524

<210> 22

<211> 668

<212> PRT

<213> feline calicivirus

<220>

<223>

<400> 1

Met Cys Ser Thr Cys Ala Asn Val Leu Lys Tyr Tyr Asp Trp Asp
1 5 10 15

Pro His Ile Lys Leu Val Ile Asn Pro Asn Lys Phe Leu His Val
20 25 30

Gly Phe Cys Asp Asn Pro Leu Met Cys Cys Tyr Pro Glu Leu Leu
35 40 45

Pro Glu Phe Gly Thr Met Trp Asp Cys Asp Gln Ser Pro Leu Gln
50 55 60

Val Tyr Leu Glu Ser Ile Leu Gly Asp Asp Glu Trp Ser Ser Thr
65 70 75

His	Glu	Ala	Ile	Asp	Pro	Val	Val	Pro	Pro	Met	His	Trp	Asp	Glu	
					80					85				90	
Ala	Gly	Lys	Ile	Phe	Gln	Pro	His	Pro	Gly	Val	Leu	Met	His	His	
					95					100				105	
Leu	Ile	Cys	Lys	Val	Ala	Glu	Gly	Trp	Asp	Pro	Asn	Leu	Pro	Leu	
					110					115				120	
Phe	Arg	Leu	Glu	Ala	Asp	Asp	Gly	Ser	Ile	Thr	Thr	Pro	Glu	Gln	
					125					130				135	
Gly	Thr	Met	Val	Gly	Gly	Val	Ile	Ala	Glu	Pro	Asn	Ala	Gln	Met	
					140					145				150	
Ser	Thr	Ala	Ala	Asp	Met	Ala	Thr	Gly	Lys	Ser	Val	Asp	Ser	Glu	
					155					160				165	
Trp	Glu	Ala	Phe	Phe	Ser	Phe	His	Thr	Ser	Val	Asn	Trp	Ser	Thr	
					170					175				180	
Ser	Glu	Thr	Gln	Gly	Lys	Ile	Leu	Phe	Lys	Gln	Ser	Leu	Gly	Pro	
					185					190				195	
Leu	Leu	Asn	Pro	Tyr	Leu	Thr	His	Leu	Ala	Lys	Leu	Tyr	Val	Ala	
					200					205				210	
Trp	Ser	Gly	Ser	Val	Asp	Val	Arg	Phe	Ser	Ile	Ser	Gly	Ser	Gly	
					215					220				225	
Val	Phe	Gly	Gly	Lys	Leu	Ala	Ala	Ile	Val	Val	Pro	Pro	Gly	Ile	
					230					235				240	
Asp	Pro	Val	Gln	Ser	Thr	Ser	Met	Leu	Gln	Tyr	Pro	His	Val	Leu	
					245					250				255	
Phe	Asp	Ala	Arg	Gln	Val	Glu	Pro	Val	Ile	Phe	Ser	Ile	Pro	Asp	
					260					265				270	
Leu	Arg	Ser	Thr	Leu	Tyr	His	Leu	Met	Ser	Asp	Thr	Asp	Thr	Thr	
					275					280				285	
Ser	Leu	Val	Ile	Met	Val	Tyr	Asn	Asp	Leu	Ile	Asn	Pro	Tyr	Ala	
					290					295				300	

Asn	Asp	Ser	Asn	Ser	Ser	Gly	Cys	Ile	Val	Thr	Val	Glu	Thr	Lys
								305						315
Pro	Gly	Pro	Asp	Phe	Lys	Phe	His	Leu	Leu	Lys	Pro	Pro	Gly	Ser
				320						325				330
Met	Leu	Thr	His	Gly	Ser	Ile	Pro	Ser	Asp	Leu	Ile	Pro	Lys	Ser
				335						340				345
Ser	Ser	Leu	Trp	Ile	Gly	Asn	Arg	Phe	Trp	Ser	Asp	Ile	Thr	Asp
				350					355					360
Phe	Val	Ile	Arg	Pro	Phe	Val	Phe	Gln	Ala	Asn	Arg	His	Phe	Asp
				365						370				375
Phe	Asn	Gln	Glu	Thr	Ala	Gly	Trp	Ser	Thr	Pro	Arg	Phe	Arg	Pro
				380					385					390
Ile	Thr	Ile	Thr	Ile	Ser	Val	Lys	Glu	Ser	Ala	Lys	Leu	Gly	Ile
				395					400					405
Gly	Val	Ala	Thr	Asp	Tyr	Ile	Val	Pro	Gly	Ile	Pro	Asp	Gly	Trp
				410					415					420
Pro	Asp	Thr	Thr	Ile	Pro	Gly	Glu	Leu	Val	Pro	Val	Gly	Asp	Tyr
				425					430					435
Ala	Ile	Thr	Asn	Gly	Thr	Asn	Asn	Asp	Ile	Thr	Thr	Ala	Ala	Gln
				440					445					450
Tyr	Asp	Ala	Ala	Thr	Glu	Ile	Arg	Asn	Asn	Thr	Asn	Phe	Arg	Gly
				455					460					465
Met	Tyr	Ile	Cys	Gly	Ser	Leu	Gln	Arg	Ala	Trp	Gly	Asp	Lys	Lys
				470					475					480
Ile	Ser	Asn	Thr	Ala	Phe	Ile	Thr	Thr	Gly	Thr	Val	Asp	Gly	Ala
				485					490					495
Lys	Leu	Ile	Pro	Ser	Asn	Thr	Ile	Asp	Gln	Thr	Lys	Ile	Ala	Val
				500					505					510
Phe	Gln	Asp	Thr	His	Ala	Asn	Lys	His	Val	Gln	Thr	Ser	Asp	Asp
				515					520					525

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Thr	Leu	Ala	Leu	Leu	Gly	Tyr	Thr	Gly	Ile	Gly	Glu	Glu	Ala	Ile
							530			535				540
Gly	Ala	Asp	Arg	Asp	Arg	Val	Val	Arg	Ile	Ser	Val	Leu	Pro	Glu
							545			550				555
Arg	Gly	Ala	Arg	Gly	Gly	Asn	His	Pro	Ile	Phe	His	Lys	Asn	Ser
							560			565				570
Ile	Lys	Leu	Gly	Tyr	Val	Ile	Arg	Ser	Ile	Asp	Val	Phe	Asn	Ser
							575			580				585
Gln	Ile	Leu	His	Thr	Ser	Arg	Gln	Leu	Ser	Leu	Asn	His	Tyr	Leu
							590			595				600
Leu	Ser	Pro	Asp	Ser	Phe	Ala	Val	Tyr	Arg	Ile	Ile	Asp	Ser	Asn
							605			610				615
Gly	Ser	Trp	Phe	Asp	Ile	Gly	Ile	Asp	Asn	Asp	Gly	Phe	Ser	Phe
							620			625				630
Val	Gly	Val	Ser	Ser	Ile	Gly	Lys	Leu	Glu	Phe	Pro	Leu	Thr	Ala
							635			640				645
Ser	Tyr	Met	Gly	Ile	Gln	Leu	Ala	Lys	Ile	Arg	Leu	Ala	Ser	Asn
							650			655				660
Ile	Arg	Ser	Val	Met	Thr	Lys	Leu							
							665							

<210> 23

<211> 262

<212> PRT

<213> feline infectious peritonitis virus

<220>

<223>

<400> 1

Met Lys Tyr Ile Leu Leu Ile Leu Ala Cys Ile Ile Ala Cys Val

DRAFT - DECODED

1	5	10	15											
Tyr	Gly	Glu	Aрг	Tyr	Cys	Ala	Met	Gln	Asp	Ser	Gly	Leu	Gln	Cys
				20					25					30
Ile	Gln	Gly	Thr	Gln	Ser	Arg	Cys	Gln	Thr	Cys	Phe	Glu	Arg	Gly
				35					40					45
Asp	Leu	Ile	Trp	His	Leu	Ala	Asn	Trp	Asn	Phe	Ser	Trp	Ser	Val
				50					55					60
Ile	Leu	Ile	Val	Phe	Ile	Thr	Val	Leu	Gln	Tyr	Gly	Arg	Pro	Gln
				65					70					75
Phe	Ser	Trp	Leu	Val	Tyr	Gly	Ile	Lys	Met	Leu	Ile	Met	Trp	Leu
				80					85					90
Leu	Trp	Pro	Ile	Val	Leu	Ala	Leu	Thr	Ile	Phe	Asn	Ala	Tyr	Ser
				95					100					105
Glu	Tyr	Gln	Val	Ser	Arg	Tyr	Val	Met	Phe	Gly	Phe	Ser	Val	Ala
				110					115					120
Gly	Ala	Val	Val	Thr	Phe	Ala	Leu	Trp	Met	Met	Tyr	Phe	Val	Arg
				125					130					135
Ser	Val	Gln	Leu	Tyr	Arg	Axg	Thr	Lys	Ser	Trp	Trp	Ser	Phe	Asn
				140					145					150
Pro	Glu	Thr	Asn	Ala	Ile	Leu	Cys	Val	Asn	Ala	Leu	Gly	Arg	Ser
				155					160					165
Tyr	Val	Leu	Pro	Leu	Asp	Gly	Thr	Pro	Thr	Gly	Val	Thr	Leu	Thr
				170					175					180
Leu	Leu	Ser	Gly	Asn	Leu	Tyr	Ala	Glu	Gly	Phe	Lys	Met	Ala	Gly
				185					190					195
Gly	Leu	Thr	Ile	Glu	His	Leu	Pro	Lys	Tyr	Val	Met	Ile	Ala	Thr
				200					205					210
Pro	Ser	Arg	Thr	Ile	Val	Tyr	Thr	Ile	Val	Gly	Lys	Gln	Leu	Lys
				215					220					225
Ala	Thr	Thr	Ala	Thr	Gly	Trp	Ala	Tyr	Tyr	Val	Lys	Ser	Lys	Ala

FEBRUARY 1980

230 235 240

Gly Asp Tyr Ser Thr Glu Ala Arg Thr Asp Asn Leu Ser Glu His
245 250 255

Glu Lys Leu Leu His Met Val
260

<210> 24

<211> 377

<212> PRT

<213> feline infectious peritonitis virus

<220>

<223>

<400> 1

Met Ala Thr Gln Gly Gln Arg Val Asn Trp Gly Asp Glu Pro Ser
1 5 10 15

Lys Arg Arg Gly Arg Ser Asn Ser Arg Gly Arg Lys Asn Asn Asp
20 25 30

Ile Pro Leu Ser Phe Tyr Asn Phe Ile Thr Leu Glu Gln Glu Ser
35 40 45

Lys Phe Trp Asn Leu Cys Pro Arg Asp Leu Val Pro Lys Gly Ile
50 55 60

Gly Asn Lys Asp Gln Gln Ile Gly Tyr Trp Asn Arg Gln Ile Arg
65 70 75

Tyr Arg Ile Val Lys Gly Gln Arg Lys Glu Leu Ala Glu Arg Trp
80 85 90

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Phe Phe Tyr Phe Leu Gly Thr Gly Phe His Ala Asp Ala Lys Phe
95 100 105

Lys Asp Lys Ile Asp Gly Val Phe Trp Val Ala Arg Asp Gly Ala
110 115 120

Met Asn Lys Pro Thr Thr Leu Gly Thr Arg Gly Thr Asn Asn Glu
125 130 135

Ser Lys Pro Leu Arg Phe Asp Gly Lys Ile Pro Pro Gln Phe Gln
140 145 150

Leu Glu Val Asn Arg Ser Arg Asn Asn Ser Arg Ser Gly Ser Gln
155 160 165

Ser Arg Ser Val Ser Arg Asn Arg Ser Gln Ser Arg Gly Arg His
170 175 180

His Ser Asn Asn Gln Asn Asn Asn Val Glu Asp Thr Ile Val Ala
185 190 195

Val Leu Glu Lys Leu Gly Val Thr Asp Lys Gln Arg Ser Arg Ser
200 205 210

Lys Pro Arg Glu Arg Ser Asp Ser Lys Pro Arg Asp Thr Thr Pro
215 220 225

Lys Asn Ala Asn Lys His Thr Trp Lys Lys Thr Ala Gly Lys Gly
230 235 240

Asp Val Thr Thr Phe Tyr Gly Ala Arg Ser Ser Ser Ala Asn Phe
245 250 255

Gly Asp Ser Asp Leu Val Ala Asn Gly Asn Ala Ala Lys Cys Tyr
260 265 270

Pro Gln Ile Ala Glu Cys Val Pro Ser Val Ser Ser Ile Ile Phe
275 280 285

Gly Ser Gln Trp Ser Ala Glu Glu Ala Gly Asp Gln Val Lys Val
290 295 300

Thr Leu Thr His Thr Tyr Tyr Leu Pro Lys Asp Asp Ala Lys Thr
305 310 315

Ser Gln Phe Leu Glu Gln Ile Asp Ala Tyr Lys Atg Pro Ser Glu
320 325 330

Val Ala Lys Asp Gln Arg Gln Arg Arg Ser Arg Ser Lys Ser Ala
335 340 345

Asp Lys Lys Pro Glu Glu Lys Ser Val Thr Leu Val Glu Ala Tyr
350 355 360

Thr Asp Val Phe Asp Asp Thr Gln Val Glu Met Ile Asp Glu Val
365 370 375

Thr Asn
377

<210> 25

<211> 642

<212> PRT

<213> feline leukemia virus

<220>

<223>

<400> 1
Met Glu Ser Pro Thr His Pro Lys Pro Ser Lys Asp Lys Thr Leu
1 5 10 15
Ser Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp
20 25 30
Ile Gly Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr
35 40 45

Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr
50 55 60
Ser Met Leu Gly Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val
65 70 75
Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Ile Val Leu
80 85 90
Asn Pro Thr Asn'Val Lys His Gly Ala Arg Tyr Ser Ser Ser Lys
95 100 105
Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln Thr Tyr
110 115 120
Pro Phe Tyr Val Cys Pro Gly His Ala Pro Ser Leu Gly Pro Lys
125 130 135
Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp
140 145 150
Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser
155 160 165
Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser
170 175 180
Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys
185 190 195
Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg
200 205 210

DRAFT

Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser
215 220 225

Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn
230 235 240

Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr
245 250 255

Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala
260 265 270

Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly
275 280 285

Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala
290 295 300

Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys
305 310 315

Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly
320 325 330

Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile
335 340 345

Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met
350 355 360

Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys
365 370 375

Thr Gln Gln Gly His Thr Gly Ala His Tyr Leu Ala Ala Pro Asn
380 385 390

Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu Thr Pro Cys Ile Ser
395 400 405

Met Ala Val Leu Asn Trp Thr Ser Asp Phe Cys Val Leu Ile Glu
410 415 420

Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr Val Tyr Thr
425 430 435

His Phe Ala Lys Ala Val Arg Phe Arg Axg Glu Pro Ile Ser Leu
 440 445 450

 Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile Ala
 455 460 465

 Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln
 470 475 480

 Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu
 485 490 495

 Glu Glu Ser Ile Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser
 500 505 510

 Glu Val Val Leu Gln Asn Arg Arg Glu Leu Asp Ile Leu Phe Leu
 515 520 525

 Gln Glu Gly Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe
 530 535 540

 Tyr Ala Asp His Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu
 545 550 555

 Arg Glu Arg Leu Lys Gln Arg Gln Gln Leu Phe Asp Ser Gln Gln
 560 565 570

 Gly Trp Phe Glu Gly Trp Phe Asn Lys Ser Pro Trp Phe Thr Thr
 575 580 585

 Leu Ile Ser Ser Ile Met Gly Pro Leu Leu Ile Leu Leu Leu Ile
 590 595 600

 Leu Leu Phe Gly Pro Cys Ile Leu Asn Arg Leu Val Gln Phe Val
 605 610 615

 Lys Asp Axg Ile Ser Val Val Gln Ala Leu Ile Leu Thr Gln Gln
 620 625 630

 Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp Arg Pro
 635 640